

#2



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/034,500

DATE: 01/17/2002

TIME: 16:04:12

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Output Set: N:\CRF3\01172002\J034500.raw

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C--> 3 <110> APPLICANT: JACOBS, Antonius A.C.
4 VERMEIJ, Paul
6 <120> TITLE OF INVENTION: LAWSONIA INTRACELLULARIS VACCINE
8 <130> FILE REFERENCE: JACOBS ET AL.
10 <140> CURRENT APPLICATION NUMBER: US/10/034,500
11 <141> CURRENT FILING DATE: 2001-12-20
13 <150> PRIOR APPLICATION NUMBER: EP00204660.5
14 <151> PRIOR FILING DATE: 2000-12-20
16 <160> NUMBER OF SEQ ID NOS: 20
18 <170> SOFTWARE: PatentIn Ver. 2.1
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21 <211> LENGTH: 656
22 <212> TYPE: DNA
23 <213> ORGANISM: Lawsonia intracellularis
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(654)
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32 1 5 10 15
34 ctt gtg gat tat tca ggc tct atg atg atg aaa cat gtt gct gtt aga 96
35 Leu Val Asp Tyr Ser Gly Ser Met Met Met Lys His Val Ala Val Arg
36 20 25 30
38 gag cct aaa ata gaa tta gca aaa gaa gct ata tta aaa att aat gcg 144
39 Glu Pro Lys Ile Glu Leu Ala Lys Glu Ala Ile Leu Lys Ile Asn Ala
40 35 40 45
42 gca atg cct aaa atg tca tat caa ggt gga tta tat act ttt gca cct 192
43 Ala Met Pro Lys Met Ser Tyr Gln Gly Gly Leu Tyr Thr Phe Ala Pro
44 50 55 60
46 tat tct gta att att ccc caa ggt tct tgg aat tca tgt gtt gcc gaa 240
47 Tyr Ser Val Ile Ile Pro Gln Gly Ser Trp Asn Ser Cys Val Ala Glu
48 65 70 75 80
50 tgt gcg gtt aat aca att aag tct gat tta gaa att ttt ggt cgt ctt 288
51 Cys Ala Val Asn Thr Ile Lys Ser Asp Leu Glu Ile Phe Gly Arg Leu
52 85 90 95
54 act cct gtg gga gac ggc ata aaa atg cat gaa aca gtc att aat caa 336
55 Thr Pro Val Gly Asp Gly Ile Lys Met His Glu Thr Val Ile Asn Gln
56 100 105 110
58 atg ccc cct cag gca gcc gtt att ctt ctc act gat ggt cat aat aat 384
59 Met Pro Pro Gln Ala Ala Val Ile Leu Leu Thr Asp Gly His Asn Asn
60 115 120 125
62 tta ggg atg aat cct gtt gag gaa gta aaa tct ata tat caa aca aat 432

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63 Leu Gly Met Asn Pro Val Glu Glu Val Lys Ser Ile Tyr Gln Thr Asn
64      130      135      140
66 cct aat gtt tgt ttt cat gta gtt tca ttt gca gat gat gct gaa ggc      480
67 Pro Asn Val Cys Phe His Val Val Ser Phe Ala Asp Asp Ala Glu Gly
68 145      150      155      160
70 aaa gca ata att gat caa att gtt gca ctt aat agt gga agt gtt ctt      528
71 Lys Ala Ile Ile Asp Gln Ile Val Ala Leu Asn Ser Gly Ser Val Leu
72      165      170      175
74 gtt gat ggt tta cag ctt cta caa aat cct gct gtt tgc caa gaa ttt      576
75 Val Asp Gly Leu Gln Leu Leu Gln Asn Pro Ala Val Cys Gln Glu Phe
76      180      185      190
78 gtt aat agt gtt ttt tgt caa gag caa att ctt gtt aca gaa gaa gtt      624
79 Val Asn Ser Val Phe Cys Gln Glu Gln Ile Leu Val Thr Glu Glu Val
80      195      200      205
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97      20      25      30
99 Glu Pro Lys Ile Glu Leu Ala Lys Glu Ala Ile Leu Lys Ile Asn Ala
100      35      40      45
102 Ala Met Pro Lys Met Ser Tyr Gln Gly Gly Leu Tyr Thr Phe Ala Pro
103      50      55      60
105 Tyr Ser Val Ile Ile Pro Gln Gly Ser Trp Asn Ser Cys Val Ala Glu
106 65      70      75      80
108 Cys Ala Val Asn Thr Ile Lys Ser Asp Leu Glu Ile Phe Gly Arg Leu
109      85      90      95
111 Thr Pro Val Gly Asp Gly Ile Lys Met His Glu Thr Val Ile Asn Gln
112      100      105      110
114 Met Pro Pro Gln Ala Ala Val Ile Leu Leu Thr Asp Gly His Asn Asn
115      115      120      125
117 Leu Gly Met Asn Pro Val Glu Glu Val Lys Ser Ile Tyr Gln Thr Asn
118      130      135      140
120 Pro Asn Val Cys Phe His Val Val Ser Phe Ala Asp Asp Ala Glu Gly
121 145      150      155      160
123 Lys Ala Ile Ile Asp Gln Ile Val Ala Leu Asn Ser Gly Ser Val Leu
124      165      170      175
126 Val Asp Gly Leu Gln Leu Leu Gln Asn Pro Ala Val Cys Gln Glu Phe
127      180      185      190
129 Val Asn Ser Val Phe Cys Gln Glu Gln Ile Leu Val Thr Glu Glu Val
130      195      200      205
132 Val Val Leu Arg Gly Val Asn Phe Ala Phe

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143 <221> NAME/KEY: CDS
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149   1           5           10           15
151 caa caa tct agt ttt atg aag ggc gat gga gat caa cgt ttt tcg cct      96
152 Gln Gln Ser Ser Phe Met Lys Gly Asp Gly Asp Gln Arg Phe Ser Pro
153           20           25           30
155 aaa caa cgt tta cgt act caa ata gac att gtt gca tca gag agt ctt      144
156 Lys Gln Arg Leu Arg Thr Gln Ile Asp Ile Val Ala Ser Glu Ser Leu
157           35           40           45
159 aag ggt gtt gta ttc ttt gaa tta ggt aag act atc tgg gga cgt ggt      192
160 Lys Gly Val Val Phe Phe Glu Leu Gly Lys Thr Ile Trp Gly Arg Gly
161           50           55           60
163 gtt gat ggt gct tct att gga aca gat ggt aaa aat gtt ata aag ctc      240
164 Val Asp Gly Ala Ser Ile Gly Thr Asp Gly Lys Asn Val Ile Lys Leu
165   65           70           75           80
167 cgt tat tcc tat gtt gat tgg gtt att cct tac aca gat gtg caa gtc      288
168 Arg Tyr Ser Tyr Val Asp Trp Val Ile Pro Tyr Thr Asp Val Gln Val
169           85           90           95
171 cgt atg ggt tta caa cct tat gtc ctt cca gga ttt gtt gca ggt tct      336
172 Arg Met Gly Leu Gln Pro Tyr Val Leu Pro Gly Phe Val Ala Gly Ser
173           100          105          110
175 aca ata tta gat gct gat gga gca ggt gtt act gtt tct gct gta ttt      384
176 Thr Ile Leu Asp Ala Asp Gly Ala Gly Val Thr Val Ser Ala Val Phe
177           115          120          125
179 aat gat tat tta ggt gct aca gct ttc tgg atg cgt gca ttg cat aaa      432
180 Asn Asp Tyr Leu Gly Ala Thr Ala Phe Trp Met Arg Ala Leu His Lys
181           130          135          140
183 aac tat gat agt aat tat gga ata tca aag cta cct aac ttt aaa ggt      480
184 Asn Tyr Asp Ser Asn Tyr Gly Ile Ser Lys Leu Pro Asn Phe Lys Gly
185   145          150          155          160
187 aca aca tta gat gta gtt gga tta act att cct gta aca ata tct gat      528
188 Thr Thr Leu Asp Val Val Gly Leu Thr Ile Pro Val Thr Ile Ser Asp
189           165          170          175
191 ata aaa att gct cca tgg ggt atg ttt gct ttt gca ggt aag aag agc      576
192 Ile Lys Ile Ala Pro Trp Gly Met Phe Ala Phe Ala Gly Lys Lys Ser
193           180          185          190
195 tta tta ggg gaa agc tat gga gat att gaa gat gta aga gca ggt ctt      624
196 Leu Leu Gly Glu Ser Tyr Gly Asp Ile Glu Asp Val Arg Ala Gly Leu
197           195          200          205
199 tta cca gca atg cca gca gga ttt gga tat agc tgg gga gct ggt aat      672

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204	Pro	Phe	Gly	Asp	Val	Phe	Pro	Asn	Lys	Lys	Arg	Gly	Asn	Ala	Trp	Trp	
205	225					230					235					240	
207	gtt	ggt	tta	tca	gct	gaa	ctt	gct	ggc	tca	agt	cct	ttg	cat	ata	gct	768
208	Val	Gly	Leu	Ser	Ala	Glu	Leu	Ala	Gly	Ser	Ser	Pro	Leu	His	Ile	Ala	
209					245					250					255		
211	gtt	gat	ggt	gct	tat	gga	cga	gca	gac	tta	gga	agt	ctt	aga	aat	gtt	816
212	Val	Asp	Gly	Ala	Tyr	Gly	Arg	Ala	Asp	Leu	Gly	Ser	Leu	Arg	Asn	Val	
213					260				265					270			
215	gtt	att	ggt	gac	ttc	tta	cta	gat	aag	att	gat	tta	aaa	cgt	caa	ggt	864
216	Val	Ile	Gly	Asp	Phe	Leu	Leu	Asp	Lys	Ile	Asp	Leu	Lys	Arg	Gln	Gly	
217			275					280					285				
219	tgg	tat	gca	gca	tta	tta	gca	gaa	tat	aaa	ttt	gaa	tat	gta	act	cca	912
220	Trp	Tyr	Ala	Ala	Leu	Leu	Ala	Glu	Tyr	Lys	Phe	Glu	Tyr	Val	Thr	Pro	
221		290					295					300					
223	ggg	gtt	ata	ggt	tgg	tat	gcc	tca	gga	gat	aaa	gtt	gat	tca	cgt	ggc	960
224	Gly	Val	Ile	Gly	Trp	Tyr	Ala	Ser	Gly	Asp	Lys	Val	Asp	Ser	Arg	Gly	
225	305					310					315					320	
227	gcc	tct	aaa	aga	ata	cca	aca	tta	gtt	gga	aac	tgg	tca	gca	aca	agt	1008
228	Ala	Ser	Lys	Arg	Ile	Pro	Thr	Leu	Val	Gly	Asn	Trp	Ser	Ala	Thr	Ser	
229					325					330					335		
231	ttt	gga	tat	agt	gga	gcc	tat	ggt	ata	ggc	aaa	gat	tct	gtt	ttt	gga	1056
232	Phe	Gly	Tyr	Ser	Gly	Ala	Tyr	Gly	Ile	Gly	Lys	Asp	Ser	Val	Phe	Gly	
233					340				345					350			
235	aat	act	att	gct	ggc	tca	tgg	ggt	gtt	gta	gtt	cag	ttg	aaa	gat	att	1104
236	Asn	Thr	Ile	Ala	Gly	Ser	Trp	Gly	Val	Val	Val	Gln	Leu	Lys	Asp	Ile	
237			355					360					365				
239	tct	ttc	tta	gaa	aat	cta	act	cat	ggt	atc	cgt	gga	gct	aga	att	cag	1152
240	Ser	Phe	Leu	Glu	Asn	Leu	Thr	His	Gly	Ile	Arg	Gly	Ala	Arg	Ile	Gln	
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243	ggt	aca	aat	aat	aaa	gac	gtt	cct	gaa	cac	tta	ggt	tta	tca	tac	gtt	1200
244	Gly	Thr	Asn	Asn	Lys	Asp	Val	Pro	Glu	His	Leu	Gly	Leu	Ser	Tyr	Val	
245	385					390					395					400	
247	act	acc	att	tat	gac	aca	cgt	ggt	ggt	gat	aat	atg	ctt	tac	tta	aca	1248
248	Thr	Thr	Ile	Tyr	Asp	Thr	Arg	Gly	Gly	Asp	Asn	Met	Leu	Tyr	Leu	Thr	
249					405					410					415		
251	aag	aaa	gat	tat	gct	tgg	gaa	gta	gat	ttt	gat	act	gaa	tat	aaa	atc	1296
252	Lys	Lys	Asp	Tyr	Ala	Trp	Glu	Val	Asp	Phe	Asp	Thr	Glu	Tyr	Lys	Ile	
253				420					425					430			
255	tat	aaa	gac	tta	agt	gta	gct	ctt	gaa	ctg	tca	tat	att	cgt	ctt	gaa	1344
256	Tyr	Lys	Asp	Leu	Ser	Val	Ala	Leu	Glu	Leu	Ser	Tyr	Ile	Arg	Leu	Glu	
257			435				440						445				
259	ctt	gat	aaa	aaa	cta	tgg	aac	ctt	caa	aga	gaa	gtt	gat	aag	aat	gcc	1392
260	Leu	Asp	Lys	Lys	Leu	Trp	Asn	Leu	Gln	Arg	Glu	Val	Asp	Lys	Asn	Ala	
261		450					455					460					
263	tat	cgt	gct	ggt	tta	aat	atg	aag	tat	caa	ttc	taa					1428
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271 <213> ORGANISM: Lawsonia intracellularis
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278   20          25          30
280 Lys Gln Arg Leu Arg Thr Gln Ile Asp Ile Val Ala Ser Glu Ser Leu
281   35          40          45
283 Lys Gly Val Val Phe Phe Glu Leu Gly Lys Thr Ile Trp Gly Arg Gly
284   50          55          60
286 Val Asp Gly Ala Ser Ile Gly Thr Asp Gly Lys Asn Val Ile Lys Leu
287   65          70          75          80
289 Arg Tyr Ser Tyr Val Asp Trp Val Ile Pro Tyr Thr Asp Val Gln Val
290   85          90          95
292 Arg Met Gly Leu Gln Pro Tyr Val Leu Pro Gly Phe Val Ala Gly Ser
293  100          105          110
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296  115          120          125
298 Asn Asp Tyr Leu Gly Ala Thr Ala Phe Trp Met Arg Ala Leu His Lys
299  130          135          140
301 Asn Tyr Asp Ser Asn Tyr Gly Ile Ser Lys Leu Pro Asn Phe Lys Gly
302 145          150          155          160
304 Thr Thr Leu Asp Val Val Gly Leu Thr Ile Pro Val Thr Ile Ser Asp
305          165          170          175
307 Ile Lys Ile Ala Pro Trp Gly Met Phe Ala Phe Ala Gly Lys Lys Ser
308          180          185          190
310 Leu Leu Gly Glu Ser Tyr Gly Asp Ile Glu Asp Val Arg Ala Gly Leu
311          195          200          205
313 Leu Pro Ala Met Pro Ala Gly Phe Gly Tyr Ser Trp Gly Ala Gly Asn
314          210          215          220
316 Pro Phe Gly Asp Val Phe Pro Asn Lys Lys Arg Gly Asn Ala Trp Trp
317 225          230          235          240
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320          245          250          255
322 Val Asp Gly Ala Tyr Gly Arg Ala Asp Leu Gly Ser Leu Arg Asn Val
323          260          265          270
325 Val Ile Gly Asp Phe Leu Leu Asp Lys Ile Asp Leu Lys Arg Gln Gly
326          275          280          285
328 Trp Tyr Ala Ala Leu Leu Ala Glu Tyr Lys Phe Glu Tyr Val Thr Pro
329          290          295          300
331 Gly Val Ile Gly Trp Tyr Ala Ser Gly Asp Lys Val Asp Ser Arg Gly
332 305          310          315          320
334 Ala Ser Lys Arg Ile Pro Thr Leu Val Gly Asn Trp Ser Ala Thr Ser
335          325          330          335
337 Phe Gly Tyr Ser Gly Ala Tyr Gly Ile Gly Lys Asp Ser Val Phe Gly

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VERIFICATION SUMMARY

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DATE: 01/17/2002

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